SPECIFICATION AMENDMENTS:

Please amend the Specification as indicated:

Please amend paragraph [0017] as follows:

[0017] FIG. 1 is a schematic diagram illustrating the preferential display technique. The figure shows the end products of unique RNA and cDNA strands isolated after degradation of the cDNA/RNA ~~compliments~~ complements. FIG 2 is a schematic diagram of the final treatment with RNase to degrade the single stranded RNA's present in each sample and the PCR amplification of the isolated cDNA which are uniquely expressed in each sample.

Please amend paragraph [0019] as follows:

[0019] The invention is a method called Preferential Display. The approach starts with the sample collection and categorizing of the cells, tissues or blood samples. Once the normalized control cells are isolated from the diseased state, expressed RNA's are isolated using standard methods. The RNA's are then placed into two tubes of normal and the other diseased RNA's for a total of four tubes. One normal and diseased are then RT-PCR with dye labeled oligos producing fluorescence labelled cDNA's in each tube. At this point of the reaction, RNA's of normal and diseased are added to their complementary tubes, normalized cDNAs with diseased RNAs and diseased cDNAs with normalized RNAs. Common sequences in each tube hybridize to form cDNA/RNA ~~compliments~~ complements. The tubes are then treated with Exonuclease III or VII to degrade all the hybridized complements. RNase is then added to digest the single stranded RNA's in each tube. The remaining undigested cDNA are unique dye labeled sequences expressed in either normal or diseased states. Additional PCR can be ran to increase the cDNA present in each tube before running on a gel or high throughput sequencer.